Amendments to Specification

In the Title, at page 2, line 2:

A NUCLEIC ACID ENCODING A WHEAT BRITTLE-1 HOMOLOG ~~BRITTLE-1 HOMOLOGS~~

Paragraph at page 1, lines 3-6:

This application is a continuation of U.S. Application No. 09/796,766, filed 1 March 2001, which is a continuation-in-part of U.S. Application No. 09/668,884, filed 25 September 2000, [[now pending,]] which is a continuation ~~claims priority benefit~~ of ~~the~~ International Application No. PCT/US99/06583, filed 22 March 1999, [[now pending,]] which claims priority benefit of U.S. Provisional Application No. 60/079,420, filed 26 March 1998.

Paragraph at page 4, line 33 to page 5, line 2:

Figure 1A and 1B depicts the amino acid sequence alignment between the brittle-1 homologs encoded by the nucleotide sequences derived from soybean clone sfl1.pk0015.h4 (SEQ ID NO:10) and wheat clone wdk1c.pk012.c23 (SEQ ID NO:18), and *Zea mays* brittle-1 protein (NCBI GenBank Identifier (GI) No. 231654; SEQ ID NO:21). Amino acids which are conserved among all and at least two sequences with an amino acid at that position are indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Paragraph at page 9, line 18 to page 10, line 3:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410 ~~*J. Mol. Biol. 215*:403-410; see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage

plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 23, line 21 to page 23, line 37:

cDNA clones encoding brittle-1 homologs were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410 ~~*J. Mol. Biol. 215*:403-410; see also www.ncbi.nlm.nih.gov/BLAST/~~) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

Paragraph at page 25, line 16 to page 25, line 20:

Figure 1A and 1B presents an alignment of the amino acid sequences set forth in SEQ ID NOs:10 and 18 and the *Zea mays* sequence (NCBI GI No. 231654; SEQ ID NO:21). The data in Table 4 represents a calculation of the percent identity

of the amino acid sequences set forth in SEQ ID NOs:10 and 18 and the *Zea mays* sequence (NCBI GI No. 231654; SEQ ID NO:21).

At page 34, line 2:

A NUCLEIC ACID ENCODING A WHEAT BRITTLE-1 HOMOLOG ~~BRITTLE-1 HOMOLOGS~~

Paragraph at page 34, line 4 to page 34, line 8:

This invention relates to an isolated nucleic acid fragment encoding a wheat brittle-1-like protein ~~homolog~~. The invention also relates to the construction of a chimeric gene encoding all or a portion of the wheat brittle-1-like protein ~~homolog~~, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the wheat brittle-1-like protein ~~homolog~~ in a transformed host cell.